

SEQUENCE LISTING

<110> Joelle THONNARD

<120> Novel Compounds

<130> BM45399

<150> 9918034.1

<151> 1999-07-30

<160> 4

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 336

<212> DNA

<213> Moraxella catarrhalis

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accatc	catta	agggcaagac	caataagcaa	gagatttcta	gtagatttgg	ttctgct	gat	180
agcatc	tctt	ttatgatagt	ggtaataaaa	tttggacata	ccgccatact	cgctccaa	ac	240
cgatg	gcaag	aaattttatc	ccttataatt	tcttttcttt	gggtgaaacc	atacagac	ca	300
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<210> 2

<211> 111

<212> PRT

<213> Moraxella catarrhalis

<400> 2

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			20					25					30		
Gln	Asn	Gln	Gln	Thr	Ile	Glu	Gln	Thr	Ile	Ile	Lys	Gly	Lys	Thr	Asn
		35					40					45			
Lys	Gln	Glu	Ile	Ser	Ser	Arg	Phe	Gly	Ser	Ala	Asp	Ser	Ile	Ser	Phe
		50				55				60					
Met	Ile	Val	Val	Ile	Lys	Phe	Gly	His	Thr	Ala	Ile	Leu	Ala	Pro	Asn
65					70				75					80	
Arg	Trp	Gln	Glu	Ile	Leu	Ser	Leu	Ile	Ile	Ser	Phe	Leu	Trp	Val	Lys
			85					90					95		
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<212> DNA

<213> Moraxella catarrhalis

<400> 3

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cctgtcgttc agcagattga tgacatttgc caagcaccag ccatgcaagc aaatctacaa      180
aatggtatca agcagtccat tcttgatgcc gtgatgagcc aaatgacgga tgcagacccc      240
aaccaacgcc tcgccatata aaataccatt ggtcagcagc tgaataacttt acaaatcacc      300
acccaaaatg ccacgaatct tgccgatagc tgtatggcgg atgtacatat aacggtaaac      360
ccccaagatt tggcgaatgc agaatttgct tttgctcggt caggggtaac tttattacag      420
cgtgctagcc aagatcaagt tgagttttat aatggcaciaa ttgtcgccaa acaaataact      480
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caggtgtcat ctgccccacg cagcgagatg tcttcaaata attcagcaca gacaccaca      780
caaaactcgg tagggcaatc ttctgcagct ggtagcacc ctcgtgtgga tcgtgatagt      840
caagccaaag ccaataaccga gcgtaccacc gagcgttctg caaataagac atctcaagac      900
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<210> 4

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<212> PRT

<213> Moraxella catarrhalis

<400> 4

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Asp Asp Glu Met Ala Val Ala Glu Pro Val Val Gln Gln Ile Asp Asp
 35          40          45
Ile Cys Gln Ala Pro Ala Met Gln Ala Asn Leu Gln Asn Gly Ile Lys
 50          55          60
Gln Ser Ile Leu Asp Ala Val Met Ser Gln Met Thr Asp Ala Asp Pro
 65          70          75          80
Asn Gln Arg Leu Ala Ile Gln Asn Thr Ile Gly Gln Gln Leu Asn Thr
 85          90          95
Leu Gln Ile Thr Thr Gln Asn Ala Thr Asn Phe Ala Asp Ser Cys Met
100          105          110
Ala Asp Val His Ile Thr Val Asn Pro Gln Asp Leu Ala Asn Ala Glu
115          120          125
Phe Ala Phe Ala Arg Ser Gly Val Thr Leu Leu Gln Arg Ala Ser Gln
130          135          140
Asp Gln Val Glu Phe Tyr Asn Gly Thr Ile Val Ala Lys Gln Ile Thr
145          150          155          160
Tyr Gln Met Val Asn Gly Asn Val Val Met Tyr Gly Asn Asn His Asn
165          170          175
Ala Ile Leu Leu Ile Ala Asp Ile Leu Ala Ala Ser Thr Ser Ser Leu
180          185          190
Pro Gln Val Ser Ile Gln Ser Asp Val Thr Ala Arg Pro Gln Ala Ile
195          200          205
Glu Arg Leu Pro Glu Ala Pro Ile Ala Met Pro Ser Asn Pro Gln Glu
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210		215		220
Asp Ser Ser Val Thr Thr Tyr Ile Glu Gln Lys Pro Ala Pro Asn Ala				
225		230		235
Gln Val Ser Ser Arg Pro Arg Ser Glu Met Ser Ser Asn Asn Ser Ala				
		245		250
Gln Thr Pro Thr Gln Asn Ser Val Gly Gln Ser Ser Ala Ala Gly Ser				
		260		265
Thr Pro Arg Val Asp Arg Asp Ser Gln Ala Lys Ala Asn Thr Glu Arg				
		275		280
Thr Thr Glu Arg Ser Ala Asn Lys Thr Ser Gln Asp Leu Pro His Pro				
		290		295
Gln Pro Pro Thr Ala Asn Ala Ser Ser Asp Gly Lys Thr Ser Ile Ser				
305		310		315
Ile Val Glu Ser Asn Glu Thr Tyr				
		325		

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